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Previously unidentified single nucleotide polymorphisms in HIV/AIDS cases associate with clinical parameters and disease progression

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Abstract

© 2016 Vladimir V. Anokhin et al.The genetic background of an individual plays an important role in the progression of HIV infection to AIDS. Identifying previously unknown or uncharacterized single nucleotide polymorphisms (SNPs) that associate with disease progression may reveal important therapeutic targets and provide a greater understanding of disease pathogenesis. In the present study, we employed ultra-high multiplex PCR on an Ion Torrent next-generation sequencing platform to sequence 23 innate immune genes from 94 individuals with HIV/AIDS. This data was used to identify potential associations of SNPs with clinical parameters and disease progression. SNPs that associated with an increased viral load were identified in the genes for the interleukin 15 receptor (IL15RA), toll-like receptor 7 (TLR7), tripartite motif-containing protein 5 (TRIM5), and two killer-cell immunoglobulin-like receptors (KIR2DL1 and KIR2DL3). Additionally, SNPs that associated with progression from HIV infection to AIDS were identified in two 2′-5′-oligoadenylate synthetase genes (OAS2 and OAS3). In contrast, other SNPs identified in OAS2 and OAS3 genes, as well as in the TRIM5 and KIR2DS4 genes, were associated with a slower progression of disease. Taken together, our data demonstrates the utility of ultra-high multiplex PCR in identifying polymorphisms of potential clinical significance and further,identifies SNPs that may play a role in HIV pathogenesis.

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